SEQUENCE LISTING

<110> Duke University
Chuan-Yuan, Li
Xiuwu, Zhang

<120> GENERATION OF RECOMBINANT ADENO-ASSOCIATED VIRAL VECTORS BY A COMPLETE ADENOVIRUS-MEDIATED APPROACH

<130> 180/137

<150> US 60/349,532
<151> 2002-01-18

<160> 22

<170> PatentIn version 3.2

<210> 1
<211> 1611
<212> DNA
<213> adeno-associated virus 2

<220>
<221> CDS
<222> (1)..(1611)

<400> 1

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gag cat ctg ccc ggc att tct gac agc ttt gtg aac tgg gtg gcc gag      96
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20                  25                  30

aag gaa tgg gag ttg ccg cca gat tct gac atg gat ctg aat ctg att     144
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45

gag cag gca ccc ctg acc gtg gcc gag aag ctg cag cgc gac ttt ctg     192
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50                  55                  60

acg gaa tgg cgc cgt gtg agt aag gcc ccg gag gcc ctt ttc ttt gtg     240
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80

caa ttt gag aag gga gag agc tac ttc cac atg cac gtg ctc gtg gaa     288
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85                  90                  95

acc acc ggg gtg aaa tcc atg gtt ttg gga cgt ttc ctg agt cag att     336
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100                 105                 110

cgc gaa aaa ctg att cag aga att tac cgc ggg atc gag ccg act ttg     384
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
        115                 120                 125

cca aac tgg ttc gcg gtc aca aag acc aga aat ggc gcc gga ggc ggg     432
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140
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aac aag gtg gtg gat gag tgc tac atc ccc aat tac ttg ctc ccc aaa      480
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

acc cag cct gag ctc cag tgg gcg tgg act aat atg gaa cag tat tta      528
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165                 170                 175

agc gcc tgt ttg aat ctc acg gag cgt aaa cgg ttg gtg gcg cag cat      576
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

ctg acg cac gtg tcg cag acg cag gag cag aac aaa gag aat cag aat      624
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195                 200                 205

ccc aat tct gat gcg ccg gtg atc aga tca aaa act tca gcc agg tac      672
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

atg gag ctg gtc ggg tgg ctc gtg gac aag ggg att acc tcg gag aag      720
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

cag tgg atc cag gag gac cag gcc tca tac atc tcc ttc aat gcg gcc      768
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

tcc aac tcg cgg tcc caa atc aag gct gcc ttg gac aat gcg gga aag      816
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260                 265                 270

att atg agc ctg act aaa acc gcc ccc gac tac ctg gtg ggc cag cag      864
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275                 280                 285

ccc gtg gag gac att tcc agc aat cgg att tat aaa att ttg gaa cta      912
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290                 295                 300

aac ggg tac gat ccc caa tat gcg gct tcc gtc ttt ctg gga tgg gcc      960
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

acg aaa aag ttc ggc aag agg aac acc atc tgg ctg ttt ggg cct gca     1008
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

act acc ggg aag acc aac atc gcg gag gcc ata gcc cac act gtg ccc     1056
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340                 345                 350

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tgt gtc gac aag atg gtg atc tgg tgg gag gag ggg aag atg acc gcc     1152
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

aag gtc gtg gag tcg gcc aaa gcc att ctc gga gga agc aag gtg cgc     1200
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400
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gtg gac cag aaa tgc aag tcc tcg gcc cag ata gac ccg act ccc gtg     1248
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415

atc gtc acc tcc aac acc aac atg tgc gcc gtg att gac ggg aac tca     1296
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

acg acc ttc gaa cac cag cag ccg ttg caa gac cgg atg ttc aaa ttt     1344
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445

gaa ctc acc cgc cgt ctg gat cat gac ttt ggg aag gtc acc aag cag     1392
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

gaa gtc aaa gac ttt ttc cgg tgg gca aag gat cac gtg gtt gag gtg     1440
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465                 470                 475                 480

gag cat gaa ttc tac gtc aaa aag ggt gga gcc aag aaa aga ccc gcc     1488
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485                 490                 495

ccc agt gac gca gat ata agt gag ccc aaa cgg gtg cgc gag tca gtt     1536
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500                 505                 510

gcg cag cca tcg acg tca gac gcg gaa gct tcg atc aac tac gca gac     1584
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
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aga ttg gct cga gga cac tct ctc tga                                1611
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<212> PRT
<213> adeno-associated virus 2

<400> 2

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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50                  55                  60

Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80
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Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85 90 95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100 105 110

Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130 135 140

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170 175

Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180 185 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195 200 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210 215 220

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
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Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
275 280 285

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305 310 315 320

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325 330 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340 345 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355 360 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370 375 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
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Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
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Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
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Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
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Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 475 480

Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
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Arg Leu Ala Arg Gly His Ser Leu
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<213> adeno-associated virus 2

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<222> (1)..(1866)

<400> 3

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1               5                  10                  15

ggg cat ctg ccc ggc att tct gac agc ttt gtg aac tgg gtg gcc gag      96
Gly His Leu Pro Gly Ile Ser Asp Ser Phe Val Asn Trp Val Ala Glu
            20                  25                  30

aag gaa tgg gag ttg ccg cca gat tct gac atg gat ctg aat ctg att     144
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45

gag cag gca ccc ctg acc gtg gcc gag aag ctg cag cgc gac ttt ctg     192
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50                  55                  60

acg gaa tgg cgc cgt gtg agt aag gcc ccg gag gcc ctt ttc ttt gtg     240
Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80

caa ttt gag aag gga gag agc tac ttc cac atg cac gtg ctc gtg gaa     288
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85                  90                  95

acc acc ggg gtg aaa tcc atg gtt ttg gga cgt ttc ctg agt cag att     336
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100                 105                 110

cgc gaa aaa ctg att cag aga att tac cgc ggg atc gag ccg act ttg     384
Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
        115                 120                 125

cca aac tgg ttc gcg gtc aca aag acc aga aat ggc gcc gga ggc ggg     432
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140

aac aag gtg gtg gat gag tgc tac atc ccc aat tac ttg ctc ccc aag     480
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

acc cag cct gaa ctg cag tgg gcg tgg act aat atg gaa cag tat tta     528
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165                 170                 175

agc gcc tgt ttg aat ctc acg gag cgt aaa cgg ttg gtg gcg cag cat     576
Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

ctg acg cac gtg tcg cag acg cag gag cag aac aaa gag aat cag aat     624
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
        195                 200                 205

ccc aat tct gat gcg ccg gtg atc aga tca aaa act tca gcc agg tac     672
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

atg gag ctg gtc ggg tgg ctc gtg gac aag ggg att acc tcg gag aag     720
Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

cag tgg ata cag gag gac cag gcc tca tac atc tcc ttc aat gcg gcc     768
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255
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tcc aac tcg cgg tcc caa atc aag gct gcc ttg gac aat gcg gga aag      816
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260                 265                 270

att atg agc ctg act aaa acc gcc ccc gac tac ctg gtg ggc cag cag      864
Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275                 280                 285

ccc gtg gag gac att tcc agc aat cgg att tat aaa att ttg gaa cta      912
Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290                 295                 300

aac ggg tac gat ccc caa tat gcg gct tcc gtc ttt ctg gga tgg gcc      960
Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

acg aaa aag ttc ggc aag agg aac acc atc tgg ctg ttt ggg cct gca     1008
Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

act acc ggg aag acc aac atc gcg gag gcc ata gcc cac act gtg ccc     1056
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
            340                 345                 350

ttc tac ggg tgc gta aac tgg acc aat gag aac ttt ccc ttc aac gac     1104
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

tgt gtc gat aag atg gtg atc tgg tgg gag gag ggg aag atg acc gcc     1152
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

aag gtc gtg gag tcg gcc aaa gcc att ctc gga gga agc aag gtg cgc     1200
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

gtg gac cag aaa tgc aag tcc tcg gcc cag ata gac ccg act ccc gtg     1248
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415

atc gtc acc tcc aac acc aat atg tgc gcc gtg att gac ggg aac tca     1296
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

acg acc ttc gaa cac cag cag ccg ttg caa gac cgg atg ttc aaa ttt     1344
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445

gaa ctc acc cgc cgt ctg gat cat gac ttt ggg aag gtc acc aag cag     1392
Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

gaa gtc aaa gac ttt ttc cgg tgg gca aag gat cac gtg gtt gag gtg     1440
Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465                 470                 475                 480

gag cat gag ttc tac gtc aaa aag ggt gga gcc aag aaa aga ccc gcc     1488
Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485                 490                 495

ccc agt gac gca gat ata agt gag ccc aaa cgg gtg cgc gag tca gtt     1536
Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500                 505                 510
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gcg cag cca tcg acg tca gac gcg gaa gct tcg atc aac tac gca gat 1584
Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525

aga tac caa aac aaa tgt tct cgt cac gtg ggc atg aat ctg atg ctg 1632
Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530 535 540

ttt ccg tgc aga caa tgc gag aga atg aat cag aac tca aat atc tgc 1680
Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545 550 555 560

ttc act cac gga cag aaa gac tgt tta gag tgc ttt ccc gtg tca gaa 1728
Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570 575

tct caa ccc gtt tct gtc gtc aaa aag gcg tat cag aaa ctg tgc tac 1776
Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590

att cat cat atc atg gga aag gtg cca gac gct tgc act gcc tgc gat 1824
Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
595 600 605

ctg gtc aat gtg gat ttg gat gac tgc atc ttt gaa caa taa 1866
Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
610 615 620

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<213> adeno-associated virus 2

<400> 4

Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35 40 45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50 55 60

Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65 70 75 80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
85 90 95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100 105 110

Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130 135 140

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
165 170 175

Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
180 185 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
195 200 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210 215 220

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225 230 235 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
275 280 285

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
290 295 300

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305 310 315 320

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325 330 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
340 345 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355 360 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370 375 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435 440 445

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460

Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465 470 475 480

Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
485 490 495

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
500 505 510

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
515 520 525

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
530 535 540

Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545 550 555 560

Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
565 570 575

Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
580 585 590

Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
595 600 605

Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
610 615 620

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<400> 5

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gctggtcggg tggctcgtgg acaaggggat tacctcggag aagcagtgga tccaggagga 180

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ccggaaaggc gggccagcag cctgcaagaa aaagattgaa ttttggtcag actggagacg 1860

cagactcagt acctgacccc cagcctctcg gacagccacc agcagccccc tctggtctgg 1920

gaactaatac gatggctaca ggcagtggcg caccaatggc agacaataac gagggcgccg 1980

acggagtggg taattcctcg ggaaattggc attgcgattc cacatggatg ggcgacagag 2040

tcatcaccac cagcacccga acctgggccc tgcccaccta caacaaccac ctctacaaac 2100

aaatttccag ccaatcagga gcctcgaacg acaatcacta ctttggctac agcacccctt 2160

gggggtattt tgacttcaac agattccact gccacttttc accacgtgac tggcaaagac 2220

tcatcaacaa caactgggga ttccgaccca agagactcaa cttcaagctc tttaacattc 2280

aagtcaaaga ggtcacgcag aatgacggta cgacgacgat tgccaataac cttaccagca 2340

cggttcaggt gtttactgac tcggagtacc agctcccgta cgtcctcggc tcggcgcatc 2400

aaggatgcct cccgccgttc ccagcagacg tcttcatggt gccacagtat ggatacctca 2460

ccctgaacaa cgggagtcag gcagtaggac gctcttcatt ttactgcctg gagtactttc 2520

cttctcagat gctgcgtacc ggaaacaact ttaccttcag ctacactttt gaggacgttc 2580

ctttccacag cagctacgct cacagccaga gtctggaccg tctcatgaat cctctcatcg 2640

accagtacct gtattacttg agcagaacaa acactccaag tggaaccacc acgcagtcaa 2700

ggcttcagtt ttctcaggcc ggagcgagtg acattcggga ccagtctagg aactggcttc 2760

ctggaccctg ttaccgccag cagcgagtat caaagacatc tgcggataac aacaacagtg 2820

aatactcgtg gactggagct accaagtacc acctcaatgg cagagactct ctggtgaatc 2880

cgggcccggc catggcaagc cacaaggacg atgaagaaaa gtttttttcct cagagcgggg 2940

ttctcatctt tgggaagcaa ggctcagaga aaacaaatgt ggacattgaa aaggtcatga 3000

ttacagacga agaggaaatc aggacaacca atcccgtggc tacggagcag tatggttctg 3060

tatctaccaa cctccagaga ggcaacagac aagcagctac cgcagatgtc aacacacaag 3120

gcgttcttcc aggcatggtc tggcaggaca gagatgtgta ccttcagggg cccatctggg 3180

caaagattcc acacacggac ggacattttc acccctctcc cctcatgggt ggattcggac 3240

ttaaacaccc tcctccacag attctcatca agaacacccc ggtacctgcg aatccttcga 3300

ccaccttcag tgcggcaaag tttgcttcct tcatcacaca gtactccacg ggacaggtca 3360

gcgtggagat cgagtgggag ctgcagaagg aaaacagcaa acgctggaat cccgaaattc 3420

agtacacttc caactacaac aagtctgtta atgtggactt tactgtggac actaatggcg 3480

tgtattcaga gcctcgcccc attggcacca gatacctgac tcgtaatctg taattgcttg 3540

ttaatcaata aaccgtttaa ttcgtttcag ttga 3574

<210> 6

<211> 312
<212> PRT
<213> adeno-associated virus 2

<400> 6

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1 5 10 15

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20 25 30

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35 40 45

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50 55 60

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100 105 110

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120 125

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155 160

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195 200 205

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210 215 220

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225 230 235 240

Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
245 250 255

Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
260 265 270

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
275 280 285

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
290 295 300

Arg Leu Ala Arg Gly His Ser Leu
305 310

<210> 7
<211> 397
<212> PRT
<213> adeno-associated virus 2

<400> 7

Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
1 5 10 15

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20 25 30

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35 40 45

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
50 55 60

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
65 70 75 80

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
85 90 95

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100 105 110

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
115 120 125

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140

```
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145                 150                 155                 160

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165                 170                 175

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180                 185                 190

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195                 200                 205

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210                 215                 220

Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
225                 230                 235                 240

Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
                245                 250                 255

Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
            260                 265                 270

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
        275                 280                 285

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
    290                 295                 300

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
305                 310                 315                 320

Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
                325                 330                 335

Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
            340                 345                 350

Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
        355                 360                 365

Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
    370                 375                 380

Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
385                 390                 395
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<210> 8
<211> 2478
<212> DNA
<213> adeno-associated virus 2

<400> 8
cagttgcgca gccatcgacg tcagacgcgg aagcttcgat caactacgca gacaggtacc 60

aaaacaaatg ttctcgtcac gtgggcatga atctgatgct gtttccctgc agacaatgcg 120

agagaatgaa tcagaattca aatatctgct tcactcacgg acagaaagac tgtttagagt 180

gctttcccgt gtcagaatct caacccgttt ctgtcgtcaa aaaggcgtat cagaaactgt 240

gctacattca tcatatcatg ggaaaggtgc cagacgcttg cactgcctgc gatctggtca 300

atgtggattt ggatgactgc atctttgaac aataaatgat ttaaatcagg tatggctgcc 360

gatggttatc ttccagattg gctcgaggac actctctctg aaggaataag acagtggtgg 420

aagctcaaac ctggcccacc accaccaaag cccgcagagc ggcataagga cgacagcagg 480

ggtcttgtgc ttcctgggta caagtacctc ggacccttca acggactcga caagggagag 540

ccggtcaacg aggcagacgc cgcggccctc gagcacgaca aagcctacga ccggcagctc 600

gacagcggag acaacccgta cctcaagtac aaccacgccg acgcggagtt tcaggagcgc 660

cttaaagaag atacgtcttt tgggggcaac ctcggacgag cagtcttcca ggcgaaaaag 720

agggttcttg aacctctggg cctggttgag gaacctgtta agacggctcc gggaaaaaag 780

aggccggtag agcactctcc tgtggagcca gactcctcct cgggaaccgg aaaggcgggc 840

cagcagcctg caagaaaaag attgaatttt ggtcagactg gagacgcaga ctcagtacct 900

gacccccagc ctctcggaca gccaccagca gccccctctg gtctgggaac taatacgatg 960

gctacaggca gtggcgcacc aatggcagac aataacgagg gcgccgacgg agtgggtaat 1020

tcctcgggaa attggcattg cgattccaca tggatgggcg acagagtcat caccaccagc 1080

acccgaacct gggccctgcc cacctacaac aaccacctct acaaacaaat ttccagccaa 1140

tcaggagcct cgaacgacaa tcactacttt ggctacagca ccccttgggg gtattttgac 1200

ttcaacagat tccactgcca cttttcacca cgtgactggc aaagactcat caacaacaac 1260

tggggattcc gacccaagag actcaacttc aagctcttta acattcaagt caaagaggtc 1320

acgcagaatg acggtacgac gacgattgcc aataacctta ccagcacggt tcaggtgttt 1380

actgactcgg agtaccagct cccgtacgtc ctcggctcgg cgcatcaagg atgcctcccg 1440

ccgttcccag cagacgtctt catggtgcca cagtatggat acctcaccct gaacaacggg 1500

agtcaggcag taggacgctc ttcatttac tgcctggagt actttccttc tcagatgctg 1560

cgtaccggaa acaactttac cttcagctac acttttgagg acgttccttt ccacagcagc 1620

tacgctcaca gccagagtct ggaccgtctc atgaatcctc tcatcgacca gtacctgtat 1680

tacttgagca gaacaaacac tccaagtgga accaccacgc agtcaaggct tcagttttct 1740

caggccggag cgagtgacat tcgggaccag tctaggaact ggcttcctgg accctgttac 1800

cgccagcagc gagtatcaaa gacatctgcg gataacaaca acagtgaata ctcgtggact 1860

ggagctacca agtaccacct caatggcaga gactctctgg tgaatccggg cccggccatg 1920

gcaagccaca aggacgatga agaaaagttt tttcctcaga gcggggttct catctttggg 1980

aagcaaggct cagagaaaac aaatgtggac attgaaaagg tcatgattac agacgaagag 2040

gaaatcagga caaccaatcc cgtggctacg gagcagtatg gttctgtatc taccaacctc 2100

cagagaggca acagacaagc agctaccgca gatgtcaaca cacaaggcgt tcttccaggc 2160

atggtctggc aggacagaga tgtgtacctt caggggccca tctgggcaaa gattccacac 2220

acggacggac attttcaccc ctctcccctc atgggtggat tcggacttaa acaccctcct 2280

ccacagattc tcatcaagaa caccccggta cctgcgaatc cttcgaccac cttcagtgcg 2340

gcaaagtttg cttccttcat cacacagtac tccacgggac aggtcagcgt ggagatcgag 2400

tgggagctgc agaaggaaaa cagcaaacgc tggaatcccg aaattcagta cacttccaac 2460

tacaacaagt ctgttaat 2478

<210> 9
<211> 735
<212> PRT
<213> adeno-associated virus 2

<400> 9

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro

115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
180 185 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser

370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
435 440 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
450 455 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465 470 475 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
485 490 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
515 520 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
530 535 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
580 585 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys

625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 10
<211> 598
<212> PRT
<213> adeno-associated virus 2

<400> 10

Met Ala Pro Gly Lys Lys Arg Pro Val Glu His Ser Pro Val Glu Pro
1 5 10 15

Asp Ser Ser Ser Gly Thr Gly Lys Ala Gly Gln Gln Pro Ala Arg Lys
20 25 30

Arg Leu Asn Phe Gly Gln Thr Gly Asp Ala Asp Ser Val Pro Asp Pro
35 40 45

Gln Pro Leu Gly Gln Pro Pro Ala Ala Pro Ser Gly Leu Gly Thr Asn
50 55 60

Thr Met Ala Thr Gly Ser Gly Ala Pro Met Ala Asp Asn Asn Glu Gly
65 70 75 80

Ala Asp Gly Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser Thr
85 90 95

Trp Met Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu
100 105 110

Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly
115 120 125

```
Ala Ser Asn Asp Asn His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
    130                 135                 140

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
145                 150                 155                 160

Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe
                165                 170                 175

Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Gln Asn Asp Gly Thr
            180                 185                 190

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
        195                 200                 205

Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys
    210                 215                 220

Leu Pro Pro Phe Pro Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
225                 230                 235                 240

Leu Thr Leu Asn Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr
                245                 250                 255

Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe
            260                 265                 270

Thr Phe Ser Tyr Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala
        275                 280                 285

His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr
    290                 295                 300

Leu Tyr Tyr Leu Ser Arg Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln
305                 310                 315                 320

Ser Arg Leu Gln Phe Ser Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln
                325                 330                 335

Ser Arg Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser
            340                 345                 350

Lys Thr Ser Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala
        355                 360                 365

Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro
    370                 375                 380
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Ala Met Ala Ser His Lys Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser
385                 390                 395                 400

Gly Val Leu Ile Phe Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp
                405                 410                 415

Ile Glu Lys Val Met Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn
            420                 425                 430

Pro Val Ala Thr Glu Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Arg
        435                 440                 445

Gly Asn Arg Gln Ala Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu
    450                 455                 460

Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile
465                 470                 475                 480

Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu
                485                 490                 495

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys
            500                 505                 510

Asn Thr Pro Val Pro Ala Asn Pro Ser Thr Thr Phe Ser Ala Ala Lys
        515                 520                 525

Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu
    530                 535                 540

Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu
545                 550                 555                 560

Ile Gln Tyr Thr Ser Asn Tyr Asn Lys Ser Val Asn Val Asp Phe Thr
                565                 570                 575

Val Asp Thr Asn Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg
            580                 585                 590

Tyr Leu Thr Arg Asn Leu
        595

<210>  11
<211>  533
<212>  PRT
<213>  adeno-associated virus 2

<400>  11
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Met Ala Thr Gly Ser Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala
1               5                  10                  15

Asp Gly Val Gly Asn Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp
            20                  25                  30

Met Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro
        35                  40                  45

Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala
    50                  55                  60

Ser Asn Asp Asn His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe
65                  70                  75                  80

Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg
                85                  90                  95

Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys
            100                 105                 110

Leu Phe Asn Ile Gln Val Lys Glu Val Thr Gln Asn Asp Gly Thr Thr
        115                 120                 125

Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser
    130                 135                 140

Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu
145                 150                 155                 160

Pro Pro Phe Pro Ala Asp Val Phe Met Val Pro Gln Tyr Gly Tyr Leu
                165                 170                 175

Thr Leu Asn Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys
            180                 185                 190

Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr
        195                 200                 205

Phe Ser Tyr Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His
    210                 215                 220

Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu
225                 230                 235                 240

Tyr Tyr Leu Ser Arg Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser
                245                 250                 255
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Arg Leu Gln Phe Ser Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser
            260                 265                 270

Arg Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys
        275                 280                 285

Thr Ser Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr
    290                 295                 300

Lys Tyr His Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala
305                 310                 315                 320

Met Ala Ser His Lys Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly
                325                 330                 335

Val Leu Ile Phe Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile
            340                 345                 350

Glu Lys Val Met Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro
        355                 360                 365

Val Ala Thr Glu Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Arg Gly
    370                 375                 380

Asn Arg Gln Ala Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro
385                 390                 395                 400

Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
                405                 410                 415

Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu Met
            420                 425                 430

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn
        435                 440                 445

Thr Pro Val Pro Ala Asn Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe
    450                 455                 460

Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile
465                 470                 475                 480

Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile
                485                 490                 495

Gln Tyr Thr Ser Asn Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val
            500                 505                 510
```

Asp Thr Asn Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr
515 520 525

Leu Thr Arg Asn Leu
530

<210> 12
<211> 145
<212> DNA
<213> adeno-associated virus 2

<400> 12
ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc 60

cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg 120

gccaactcca tcactagggg ttcct 145

<210> 13
<211> 144
<212> DNA
<213> adeno-associated virus 2

<400> 13
ggaaccccta gtgatggagt tggccactcc ctctctgcgc gctcgctcgc tcactgaggc 60

cgggcgacca aaggtcgccc gacgcccggg ctttgcccgg gcggcctcag tgagcgagcg 120

agcgcgcaga gagggagtgg ccaa 144

<210> 14
<211> 31
<212> DNA
<213> adeno-associated virus

<220>
<221> misc_feature
<222> (1)..(31)
<223> corresponds to base pairs 318-339 of AAV with an EcoR V site at the 5' end

<400> 14
gatatcgcca tgccggggtt ttacgagatt g 31

<210> 15
<211> 35
<212> DNA
<213> adeno-associated virus

<220>
<221> misc_feature
<222> (1)..(35)
<223> corresponds to base pairs 1812 to 1846 of AAV

<220>
<221> mutation

<222> (20)..(20)

<220>
<221> mutation
<222> (23)..(23)

<400> 15
gcacccgttt gggctcactg atgtctgcgt cactg 35

<210> 16
<211> 35
<212> DNA
<213> adeno-associated virus

<220>
<221> misc_feature
<222> (1)..(35)
<223> corresponds to base pairs 1812 to 1846 of AAV

<220>
<221> mutation
<222> (13)..(13)

<220>
<221> mutation
<222> (16)..(16)

<400> 16
cagtgacgca gacatcagtg agcccaaacg ggtgc 35

<210> 17
<211> 29
<212> DNA
<213> adeno-associated virus

<220>
<221> misc_feature
<222> (1)..(29)
<223> corresponds to base pairs 2261 to 2289 of AAV

<400> 17
tgggccaggt ttgagcttcc accactgtc 29

<210> 18
<211> 55
<212> DNA
<213> adeno-associated virus

<220>
<221> misc_feature
<222> (1)..(27)
<223> corresponds to base pairs 2261-2289 of AAV

<220>
<221> misc_feature
<222> (28)..(53)
<223> corresponds to base pairs 4330-4355 of AAV

<400> 18
gacagtggtg gaagctcaaa cctggcccaa gcacctgaat ggcacctatg attac 55

<210> 19
<211> 28
<212> DNA
<213> adeno-associated virus

<220>
<221> misc_feature
<222> (1)..(28)
<223> corresponds to base pairs 4446-4467 of AAV with a BamHI site at the 3' end

<400> 19
ggatcccgca gagaccaaag ttcaactg 28

<210> 20
<211> 27
<212> DNA
<213> adeno-associated virus

<220>
<221> misc_feature
<222> (1)..(27)
<223> corresponds to base pairs 1852 to 1878, BamHI site at the 5' end

<400> 20
agtcagttgc gcagccatcg acgtcag 27

<210> 21
<211> 35
<212> DNA
<213> adeno-associated virus

<220>
<221> misc_feature
<222> (1)..(35)
<223> corresponds to base pairs 4302 to 4329, with a Not I site at the 3' end

<400> 21
gcggccgctt aacagacttg ttgtagttgg aagtg 35

<210> 22
<211> 592
<212> DNA
<213> Homo sapiens

<400> 22
gcgtgaagag ctgcagtgtc actcttaaag ctgaattaat ctctgccatt ccttaaggaa 60

acaggcaact gtcttaaaac cgtggtttgg aaaatatttt gttcaagata aaactgtttt 120

aagatatatg tatatatatc ttatatatct gtattcgcat ggtaacatat cttcggtctt 180

cctgccgctg ggctctcagc ggccctccaa ggcagcccgc aggcccgtgc tcgcctcagg 240

gatcctccac agccccgggg agaccttgcc tctaaagttg ctgcttttgc agctctgcca 300

caaccgcgcg tcctcagagc cagccgggag gagctagaac cttccccgcg tttctttcag 360

cagccctgag tcagaggcgg gctggccttg caagtagccg cccagccttc ttcggtctca 420

cggaccgatc cgcccgaacc ttctcccggg gtcagcgccg cgctgcgccg cccggctgac 480

tcagcccggg cgggcgggcg ggaggctctc gactgggcgg gaaggtgcgg gaaggttcgc 540

ggcggcgggg tcggggaggt gcaaaaggat gaaaagcccg tggacggagc tg 592